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We claim:

1. A synthetic fatty acid desaturase gene for
5 expression in a multicellular plant, the gene comprising a
desaturase domain and a cyt b₅ domain, wherein the gene is
customized for expression in a plant cytoplasm.
2. The synthetic gene of claim 1, customized
10 from a naturally occurring gene encoding a cytosolic Δ-9
desaturase.
3. The synthetic gene of claim 2, customized
15 from a naturally occurring gene from *Saccharomyces*
cerevisiae.
4. The synthetic gene of claim 3, customized
from a naturally occurring gene from *Saccharomyces*
20 *cerevisiae* that encodes SEQ ID NO:2.
5. The synthetic gene of claim 4, customized
from a naturally occurring gene from *Saccharomyces*
cerevisiae comprising SEQ ID NO:1.
- 25 6. The synthetic gene of claim 3, comprising SEQ
ID NO:3.
7. The synthetic gene of claim 1, which further
comprises an expression regulatory sequence from a plant
30 gene encoding an ER biosynthetic pathway enzyme.
8. The synthetic gene of claim 1, customized for
expression in a monocotyledonous plant.

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9. The synthetic gene of claim 1, customized for expression in a dicotyledonous plant.

10. The synthetic gene of claim 1, customized for expression in a plant genus selected from the group consisting of *Arabidopsis*, *Brassica*, *Phaseolus*, *Oryza*, *Olea*, *Elaeis* (Oil Palm) and *Zea*.

11. The synthetic gene of claim 1, customized from a naturally occurring gene comprising both a desaturase domain and a cyt b₅ domain.

12. The synthetic gene of claim 1, wherein the gene is a chimeric gene comprising a desaturase domain and a heterologous cyt b₅ domain.

13. The synthetic gene of claim 1, customized from a naturally occurring gene such that the synthetic gene and the naturally occurring gene encode an identical amino acid sequence.

14. The synthetic gene of claim 13, wherein the synthetic gene and the naturally occurring gene encode SEQ ID NO:2.

15. The synthetic gene of claim 1, customized from a naturally occurring gene such that the synthetic gene and the naturally occurring gene encode a similar amino acid sequence.

16. The synthetic gene of claim 1, customized from a naturally occurring gene such that the synthetic gene and the naturally occurring gene encode a similar

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amino acid sequence, and the synthetic gene possesses improved stability or catalytic activity as compared with the naturally occurring gene.

5 ~~343~~ 17. A method for constructing a customized bifunctional desaturase/cyt b₅ encoding gene for expression in the cytosol of a multicellular plant, comprising the steps of:

10 (a) providing a DNA molecule comprising a desaturase-encoding moiety operably linked to a cyt b₅-encoding moiety, said DNA molecule producing the bifunctional polypeptide in a non-customized form;

15 (b) back-translating the polypeptide sequence using preferred codons for expression in a multicellular plant, thereby producing a back-translated nucleotide sequence;

(c) analyzing the back-translated nucleotide sequence for features that could diminish or prevent expression in the plant cytoplasm;

20 (d) modifying the analyzed sequence to correct or remove the features that could diminish or prevent expression in the plant cytoplasm; and

25 (e) optionally, introducing pre-determined cloning features into the sequence in a manner that does not materially affect the codon usage or final polypeptide sequence, thereby producing the customized bifunctional desaturase/cyt b₅ encoding gene for expression in the cytosol of a multicellular plant.

30 18. The method of claim 17, wherein the features that could diminish or prevent expression in the plant cytoplasm include one or more features selected from the group consisting of: putative intron splice sites, plant

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polyadenylation signals, RNA polymerase II termination sequences, and hairpin consensus sequences.

19. The method of claim 17, which further
5 comprises the step of:

(f) testing the customized bifunctional
desaturase/cyt b₅ encoding gene for desaturase function in
fatty acid deficient strains of a microorganism prior
introducing the gene into vectors for expression in plants.
10

20. The method of claim 19, wherein the
microorganism is *Saccharomyces cerevisiae*.

21. The method of claim 17, which further
15 comprises incorporating into the customized gene one or
more genomic segments from plant desaturase or other ER
lipid biosynthetic genes, which comprise beneficial
elements to further optimize expression of the genes in
plants, comprising the steps of:

- 20 a) selecting a cDNA sequence that
potentially comprises one or more of the beneficial
elements;
- b) creating a yeast vector expressing a
desaturase gene modified to contain one or more of the
25 beneficial elements;
- c) testing the vector in a yeast expression
system;
- d) isolating regions from genomic DNA that
are homologous to the beneficial elements from the cDNA;
30 and
- e) operably linking the genomic DNA regions
to the customized bifunctional desaturase/cyt b₅ encoding
gene to produce the further customized gene.